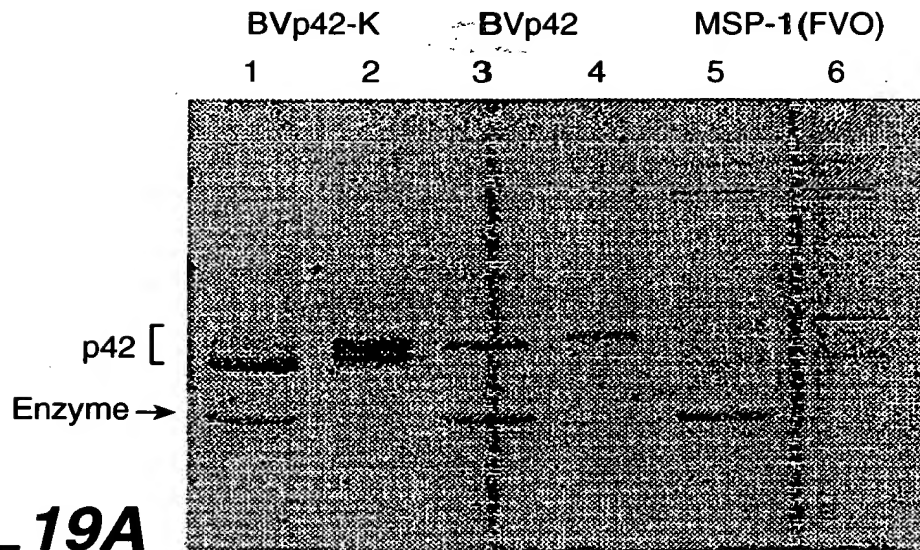
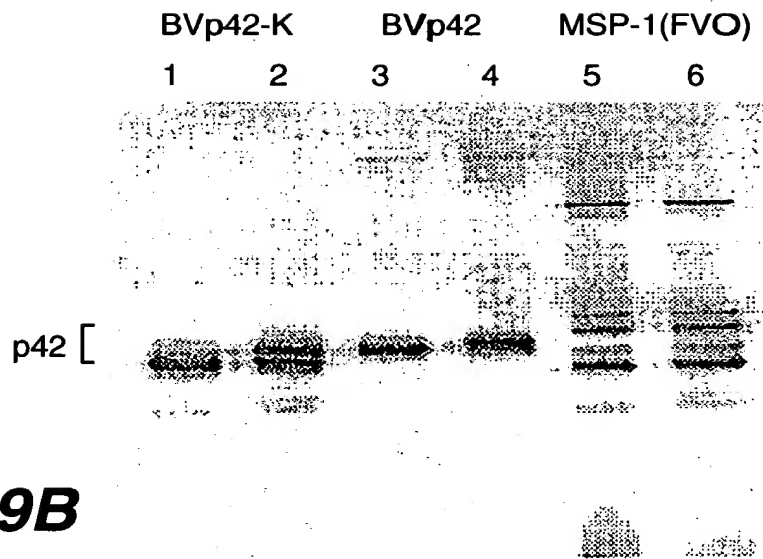
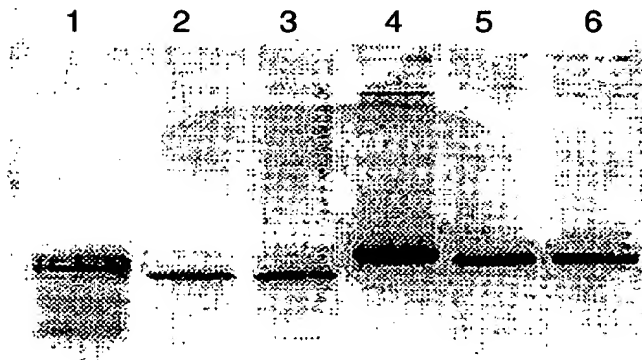
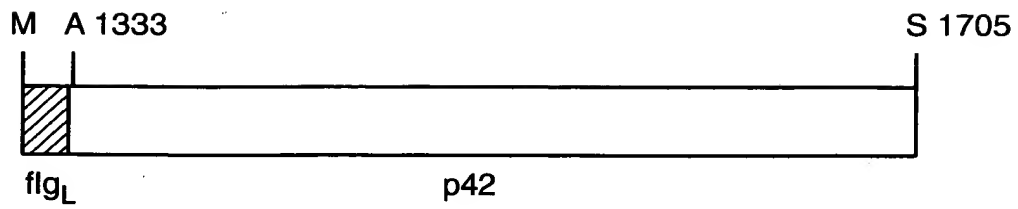
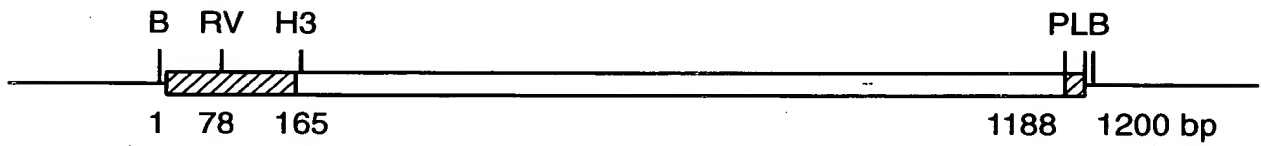
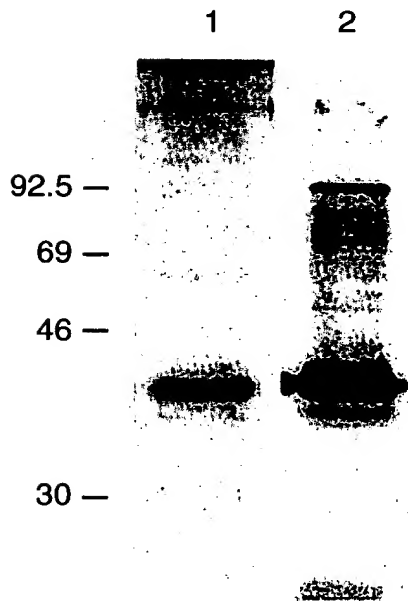
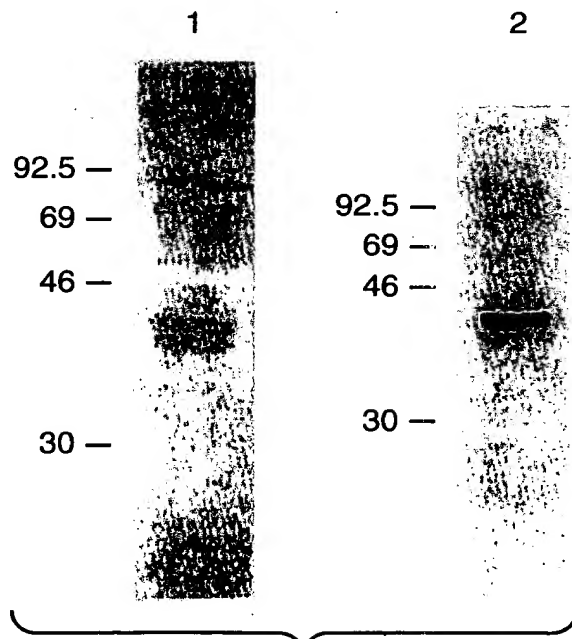
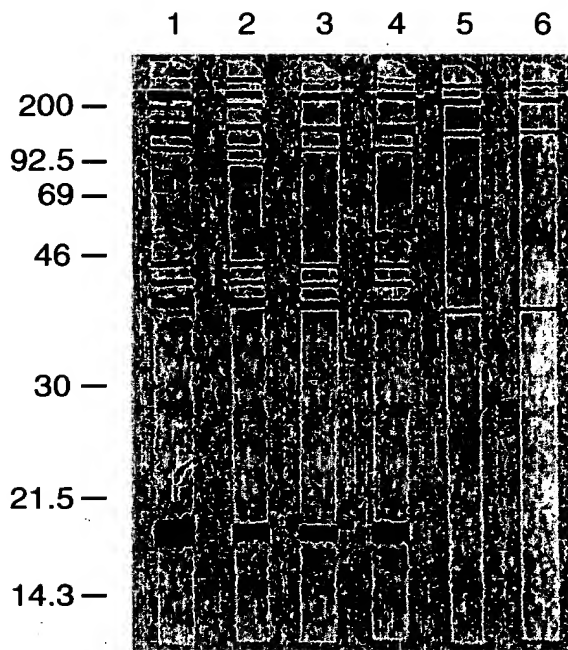
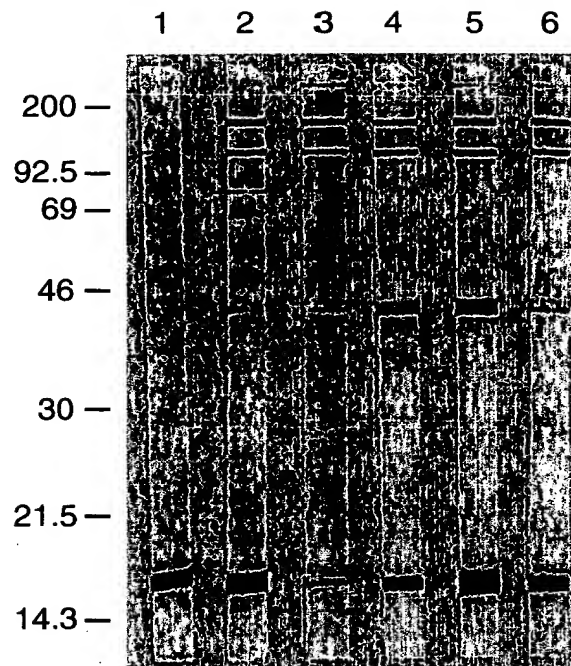
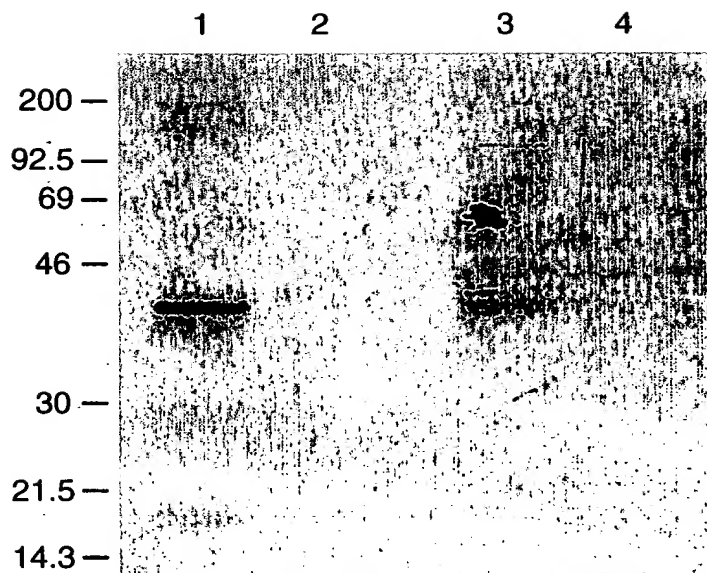
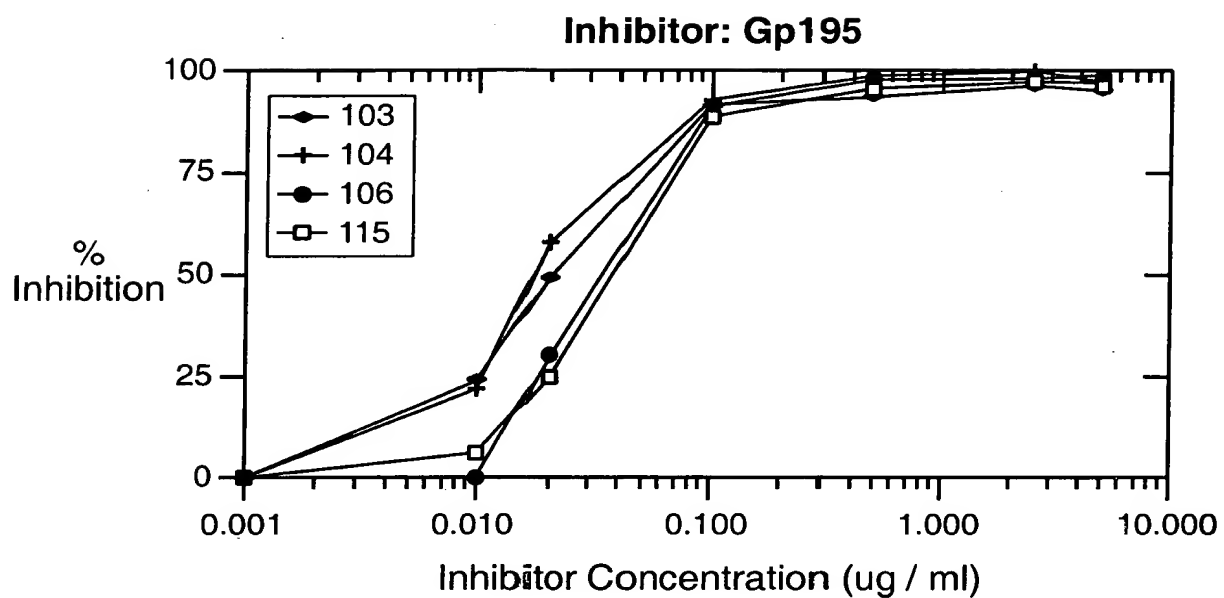
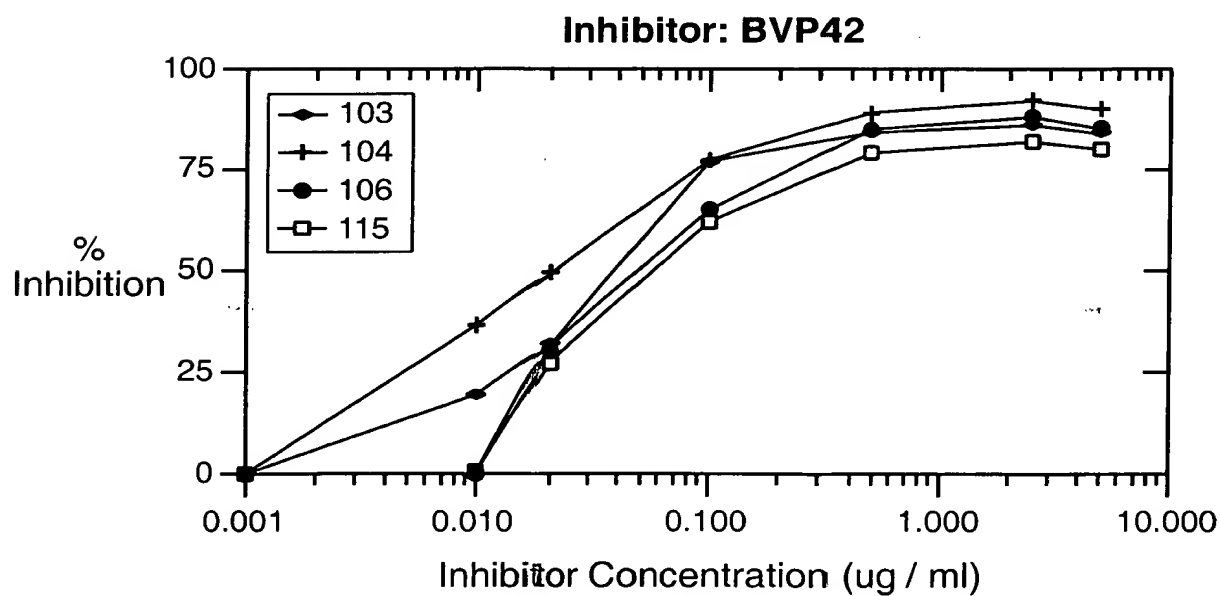


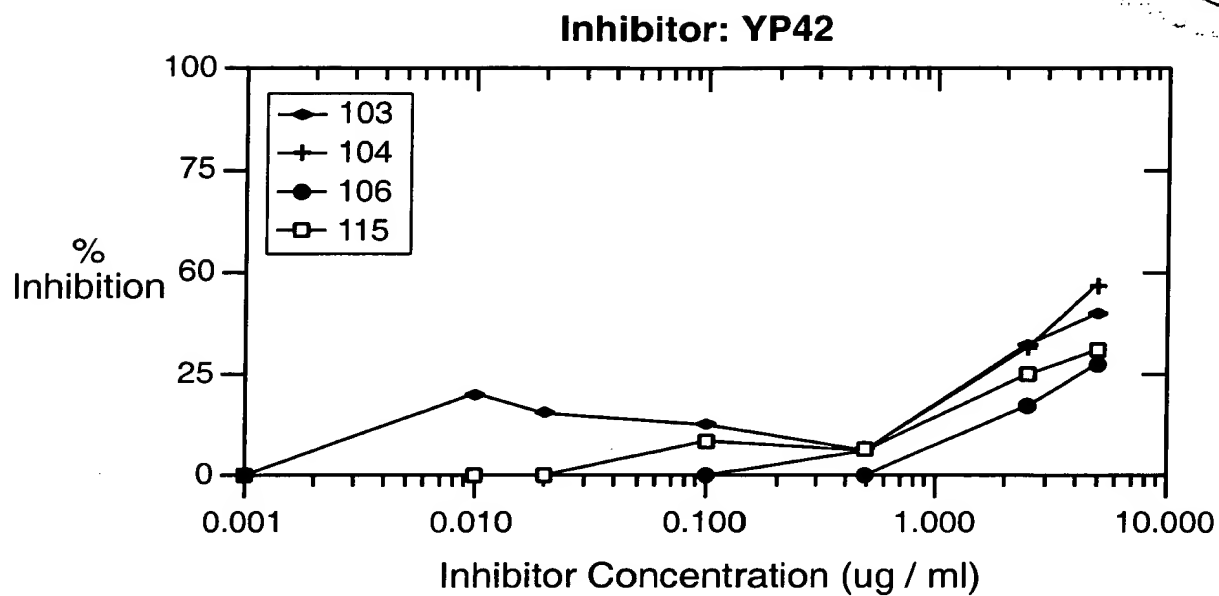
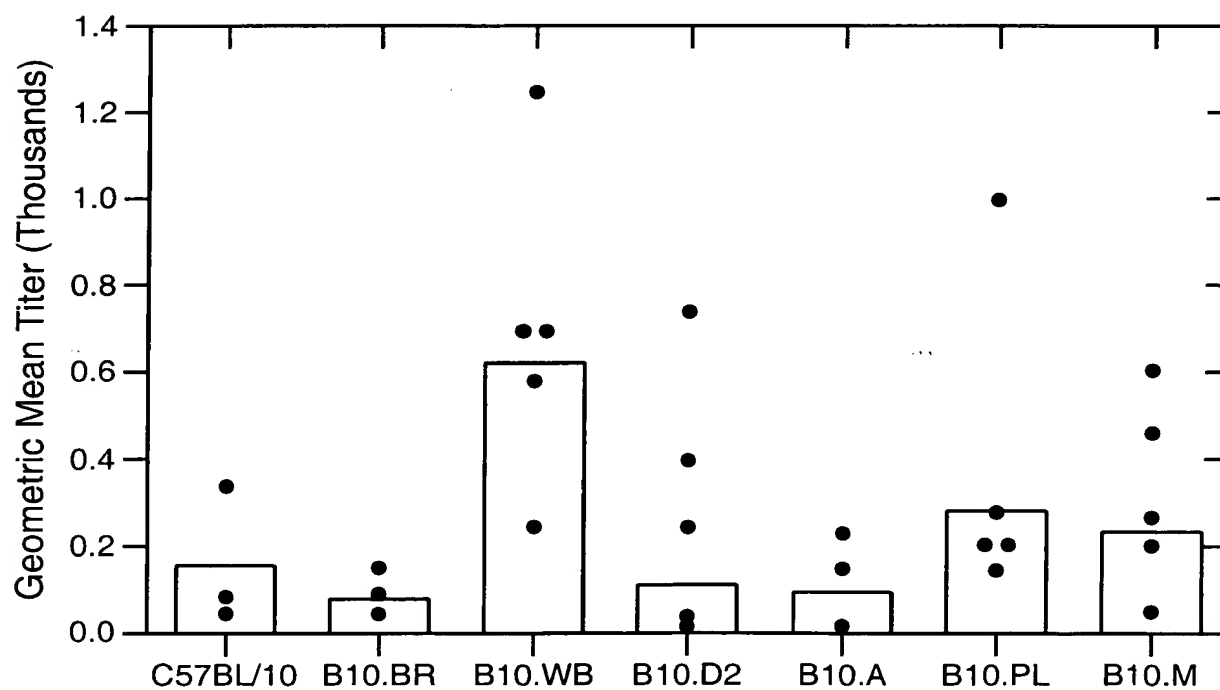
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**FIG._19A****FIG._19B****FIG._20**

**FIG._1A****FIG._1B****FIG._2A****FIG._2B**

**FIG._3A****FIG._3B****FIG._3C**

**FIG._4A****FIG._4B**

**FIG._4C****FIG._5**

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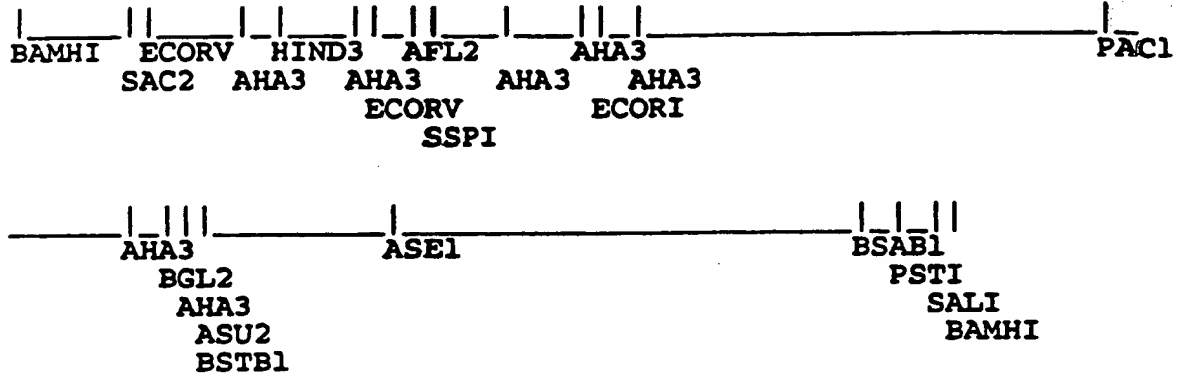


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MAD											1377											
WEL	VTTSVI	KI	E L		L N	VM	V VK	FN	EN	KN	I 1384											
K1	VTPSVIH	KI	E L		L N	VM	V VK	PFN	EN	KN	I 1325											
FUP	QFKHSSNEYIEDSF	KLNS	EQKNTLLK	SYK	IKES	VEND	IKFA	QEGIS	YVEK	VLAKYK	ODLES	IKKVIK 1473										
MAD											1448											
WEL	PY DLT	SN	VVK	PY F	K K	RDKF	S N	D	IDT	N	NDVLG	KILSE S D Y N 1405										
K1	PY DLT	SN	VVK	PY F	K K	RDKF	S N	D	IDT	N	NDVLG	KILSE S D Y N 1396										
FUP	EEKEKFPSPPT	TPPS	PAKTDEQ	KESK	FLP	FLTN	IE	TLN	LVN	KID	DY	LN	LKAK	INDC	NVEK	DEAHVK 1544						
MAD																1519						
WEL				K	GENE	Y N		KTVND	LFV	H E	VLNYTY	SNVE			1456						
K1				K	GENE	Y N		KTVND	LFV	H E	VLNYTY	SNVE			1447						
FUP	ITKLSDLKAID	KID	LFKN	ND	FEA	IKKL	IND	DTKK	DM	LG	KL	ST	GLV.QN	FPNT	II	SK	LEGK	FQDML.N 1613				
MAD																		1588				
WEL	KE NY	T Q	LAD	KN	N	VG	AD	ST	YN	HNNL	T F	M	FE	LLKS	V L	N	LDW	LARYVKH 1527				
K1	KE IY	T Q	LAD	KN	N	VG	AD	ST	YN	HNNL	T F	M	FE	LLKS	L N	LDW	LARYVKH 1518					
FUP	ISQHQC	VKKQ	CPEN	SGCF	RH	LD	ERE	CKCL	LN	VYQ	EG	DK	CV	EN	PN	PTC	NEN	NGG	DADAK	CTE	EDSG	SN GK 1684
MAD																					1659	
WEL	FTTPMRK	THIQQS																			1598	
K1	FTTPMRK	THIQQ																			1589	
FUP	KITCE	TKP	DSY	PL	FDG	IFC	SSN	FLG	IS	FL	IL	ML	IL	YS	FI							1726
MAD																					1701	
WEL																					1640	
K1																					1631	

FIG.-6



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MetTrpSerTrpLysCysLeuLeuPheTrpAlaValLeuValThrAla
 1 GGATCCACTGGGATGTGGAGCTGGAAGTGCCTCCTCTTCTGGGCTGTCCTGGTCACAGCC
 CCTAGGTGACCCTACACCTCGACCTTCACGGAGGAGAAGACCCGACAGGACCAGTGTCCGG
 1 BAMHI,
 ThrLeuCysThrAlaAlaIleSerValThrMetAspAsnIleLeuSerGlyPheGluAsn
 61 ACACTCTGCACCGCGGCGATATCTGTACAATGGATAATATCCTCTCAGGATTTGAAAT
 TGTGAGACGTGGCGCCGCTATAGACAGTGTACCTATTATAGGAGAGTCCTAACTTTTA
 71 SAC2, 78 ECORV,
 GluTyrAspValIleTyrLeuLysProLeuAlaGlyValTyrArgSerLeuLysLysGln
 121 GAATATGATGTTATATATTTAAACCTTTAGCTGGAGTATATAGAAGCTTAAAAAACAA
 CTTATACTACAATATATAAATTTTGAAATCGACCTCATATATCTTCGAATTTTTTTGTT
 138 AHA3, 165 HIND3,
 IleGluLysAsnIlePheThrPheAsnLeuAsnLeuAsnAspIleLeuAsnSerArgLeu
 181 ATTGAAAAAACATTTTACATTTAAATTTGAACGATATCTTAAATTCACGTCTT
 TAACTTTTTTTGTAAAAATGTAAATTTAAACTTGCTATAGAATTTAAGTGCAGAA
 207 AHA3, 220 ECORV, 238 AFL2,
 LysLysArgLysTyrPheLeuAspValLeuGluSerAspLeuMetGlnPheLysHisIle
 241 AAGAAACGAAAATATTTCTTAGATGTATTAGAATCTGATTTAATGCAATTTAAACATATA
 TTCTTTGCTTTTATAAAGAATCTACATAATCTTAGACTAAATTACGTTAAATTTGTATAT
 251 SSPI, 289 AHA3,
 SerSerAsnGluTyrIleIleGluAspSerPheLysLeuLeuAsnSerGluGlnLysAsn

FIG. 7A



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301 TCCTCAAATGAATACATTATTGAAGATTCATTTAAATTATTGAATTCAGAACAAAAAAC
AGGAGTTTACTTATGTAATAACTTCTAAGTAAATTTAATAACTTAAGTCTTGTTTTTTTG

331 AHA3, 342 ECORI,

361 ThrLeuLeuLysSerTyrLysTyrIleLysGluSerValGluAsnAspIleLysPheAla
ACACTTTTAAAAAGTTACAAATATATAAAAGAATCAGTAGAAAATGATATTAAATTTGCA
TGTGAAAATTTTCAATGTTTATATATTTTCTTAGTCATCTTTACTATAATTTAAACGT

366 AHA3,

421 GlnGluGlyIleSerTyrTyrGluLysValLeuAlaLysTyrLysAspAspLeuGluSer
CAGGAAGGTATAAGTTATTATGAAAAGGTTTTAGCGAAATATAAGGATGATTTAGAATCA
GTCCTTCCATATTCAATAATACTTTTCCAAAATCGCTTTATATTCCTACTAAATCTTAGT

481 IleLysLysValIleLysGluGluLysGluLysPheProSerSerProProThrThrPro
ATTAAAAAGTTATCAAAGAAGAAAAGGAGAAGTTCCCATCATCACCACCAACAACACCT
TAATTTTTTCAATAGTTTCTTCTTTTCTTCAAGGGTAGTAGTGGTGGTTGTTGTGGA

541 ProSerProAlaLysThrAspGluGlnLysLysGluSerLysPheLeuProPheLeuThr
CCGTCACCAGCAAAAACAGACGAACAAAAGAAGGAAAGTAAGTTCCTTCCATTTTAAACA
GGCAGTGGTCGTTTTTGTCTGCTTGTTTTCTTCTTTCATTCAAGGAAGGTAAAATTGT

601 AsnIleGluThrLeuTyrAsnAsnLeuValAsnLysIleAspAspTyrLeuIleAsnLeu
AACATTGAGACCTTATACAATACTTAGTTAATAAAATTGACGATTACTTAATTAACCTTA
TTGTAACCTCTGGAATATGTTATTGAATCAATTATTTTAACTGCTAATGAATTAATTGAAT

649 PAC1,

661 LysAlaLysIleAsnAspCysAsnValGluLysAspGluAlaHisValLysIleThrLys
AAGGCAAAGATTAAACGATTGTAATGTTGAAAAAGATGAAGCACATGTTAAATAACTAAA
TTCCGTTTCTAATTGCTAACATTACAACTTTTTCTACTTCGTGTACAATTTTATTGATTT

721 LeuSerAspLeuLysAlaIleAspAspLysIleAspLeuPheLysAsnHisAsnAspPhe
CTTAGTGATTTAAAAGCAATTGATGACAAAATAGATCTTTTTTAAAACCATAACGACTTC
GAATCACTAAATTTTCGTTAACTACTGTTTTATCTAGAAAAATTTTGGTATTGCTGAAG

729 AHA3, 753 BGL2, 760 AHA3, 778 ASU2 BSTB1,

781 GluAlaIleLysLysLeuIleAsnAspAspThrLysLysAspMetLeuGlyLysLeuLeu
GAAGCAATTAAAAATTGATAATGATGATACGAAAAAGATATGCTTGCGCAAATTACTT
CTTCGTAAATTTTTTAACTATTTACTACTATGCTTTTTTCTATACGAACCGTTTAATGAA

841 SerThrGlyLeuValGlnAsnPheProAsnThrIleIleSerLysLeuIleGluGlyLys
AGTACAGGATTAGTTCAAAATTTTCTAATACAATAATATCAAAATTAATTGAAGGAAAA
TCATGTCCTAATCAAGTTTTTAAAGGATTATGTTATTATAGTTTTAATTAACCTTCCTTTT

885 ASE1,

901 PheGlnAspMetLeuAsnIleSerGlnHisGlnCysValLysLysGlnCysProGluAsn
TTCCAAGATATGTTAAACATTTCAACACCAATGCGTAAAAACAATGTCCAGAAAAT
AAGGTTCTATACAATTTGTAAAGTGTTGTGGTTACGCATTTTTTTGTTACAGGTCTTTTA

961 SerGlyCysPheArgHisLeuAspGluArgGluGluCysLysCysLeuLeuAsnTyrLys
TCTGGATGTTTCAGACATTTAGATGAAAGAGAAGAATGTAAATGTTTATTAAATTACAAA
AGACCTACAAAGTCTGTAAATCTACTTCTCTTCTTACATTTACAAATAATTTAATGTTT

FIG. 7B



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1021 GlnGluGlyAspLysCysValGluAsnProAsnProThrCysAsnGluAsnAsnGlyGly
CAAGAAGGTGATAAATGTGTTGAAAATCCAAATCCTACTTGTAACGAAAATAATGGTGG
GTTCTTCCACTATTTACACAACCTTTTAGGTTTAGGATGAACATTGCTTTTATTACCACCT

1081 CysAspAlaAspAlaLysCysThrGluGluAspSerGlySerAsnGlyLysLysIleThr
TGTGATGCAGATGCCAAATGTACCGAAGAAGATTTCAGGTAGCAACGGAAAAGAAAATCACA
ACACTACGTCTACGGTTTACATGGCTTCTTCTAAGTCCATCGTTGCCTTTCTTTTAGTGT

1141 CysGluCysThrLysProAspSerTyrProLeuPheAspGlyIlePheCysSerAM AM
TGTGAATGTACTAAACCTGATTCTTATCCACTTTTCGATGGTATTTTCTGCAGTTAGTAG
ACACTTACATGATTTGGACTAAGAATAGGTGAAAAGCTACCATAAAAGACGTCAATCATC

1159 BSAB1, 1188 PSTI, 1200 SALI,

1201 TCGACCCTTGGAAGGATCC
AGCTGGGAACCTTCCTAGG

1214 BAMHI,

1261

FIG._7C

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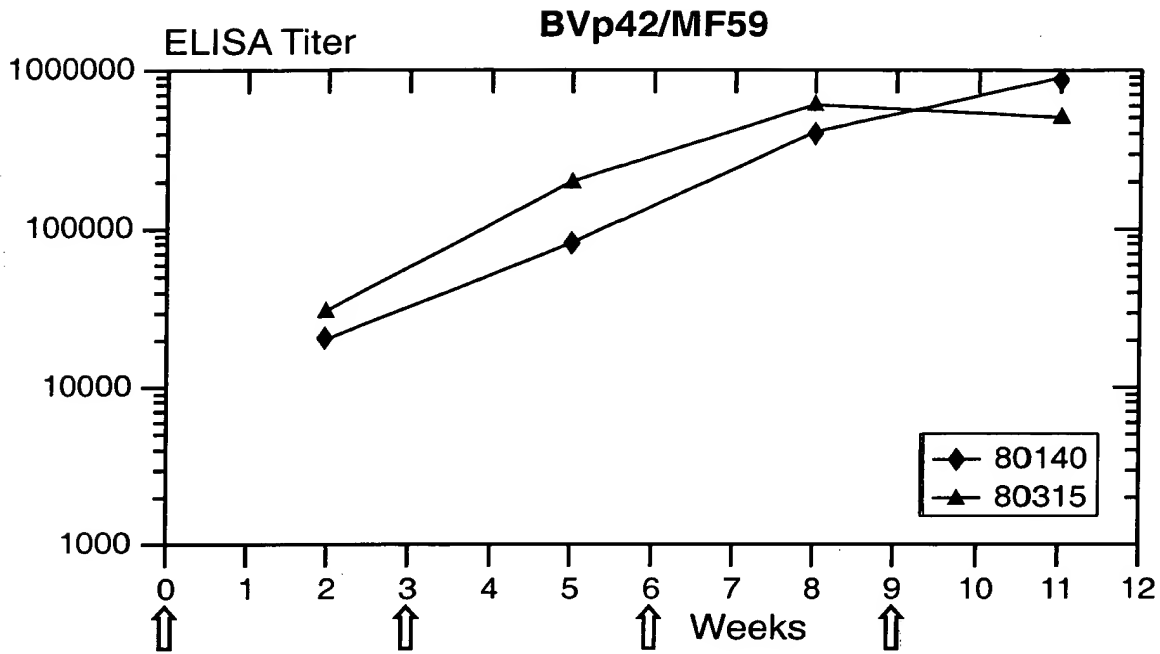


FIG._8A

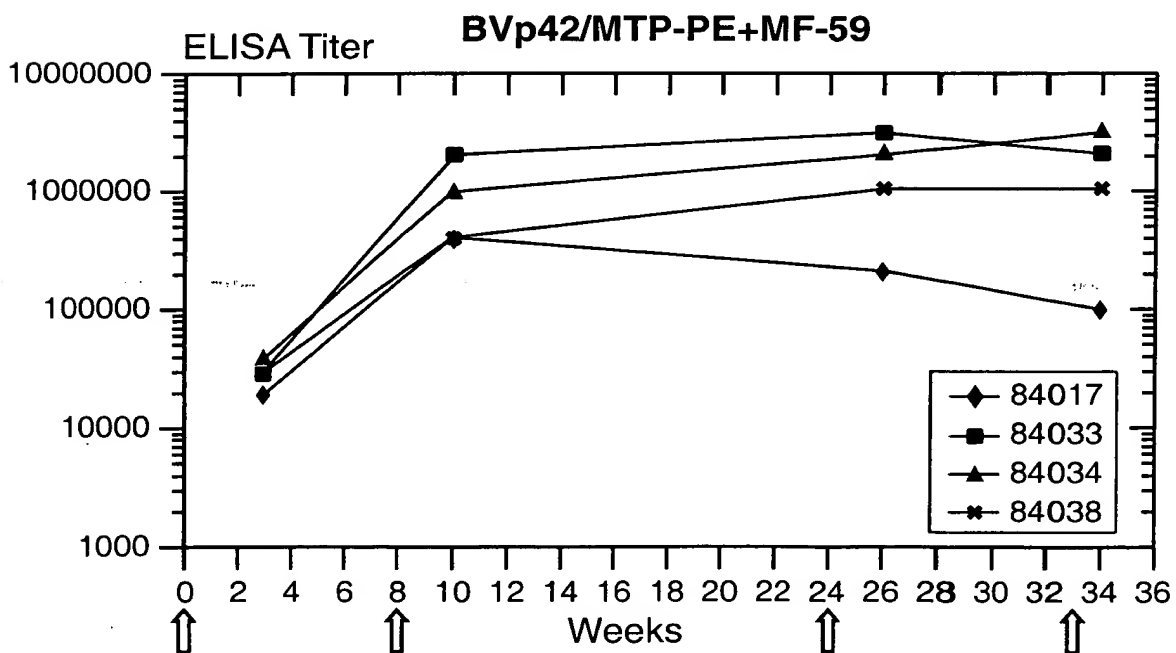


FIG._8B

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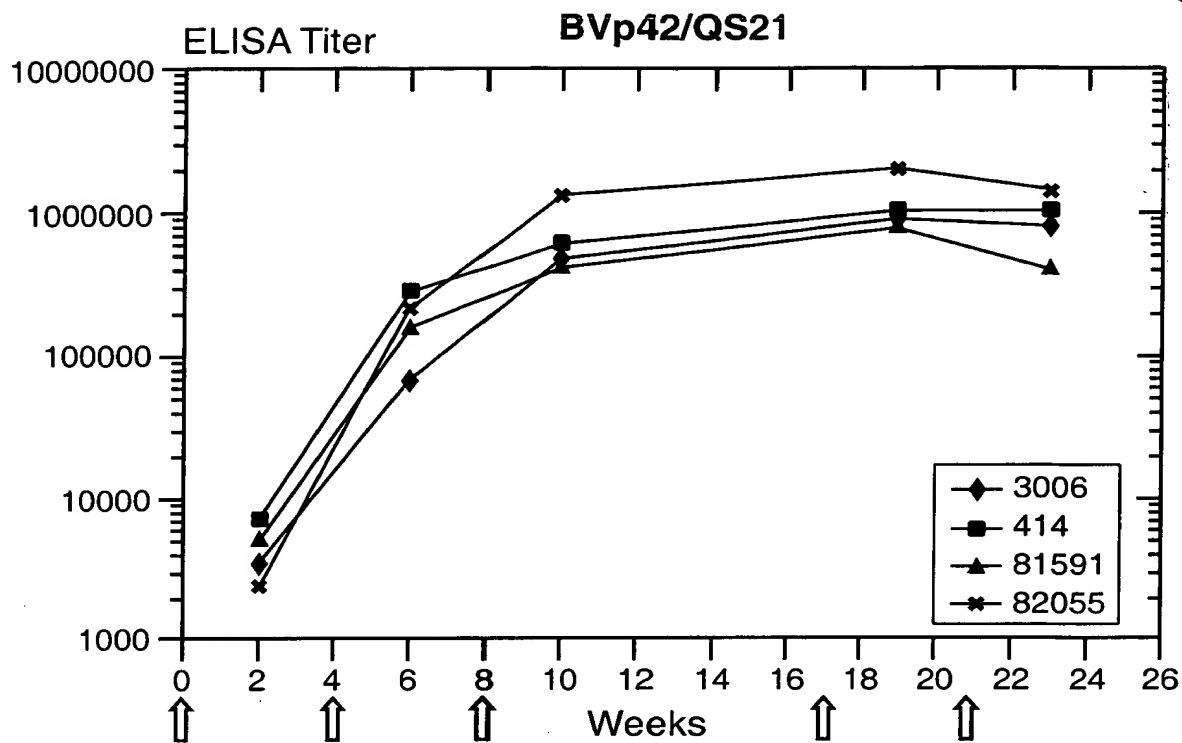


FIG._8C

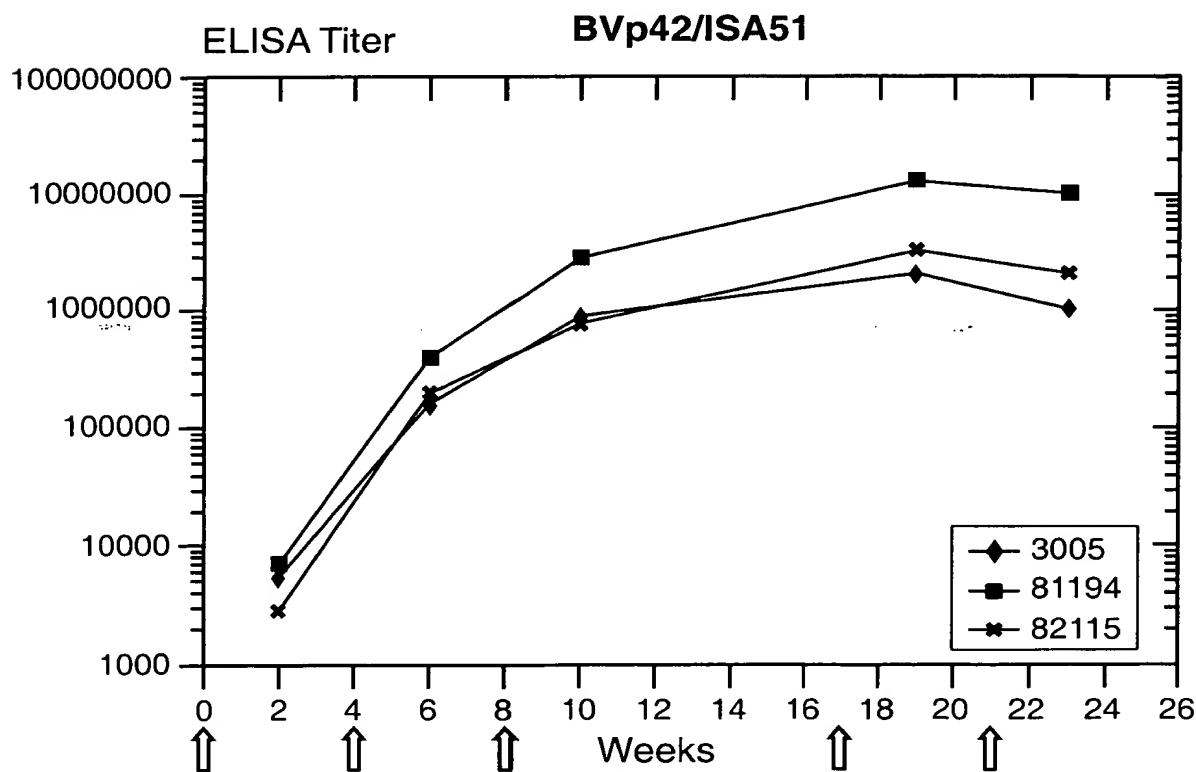
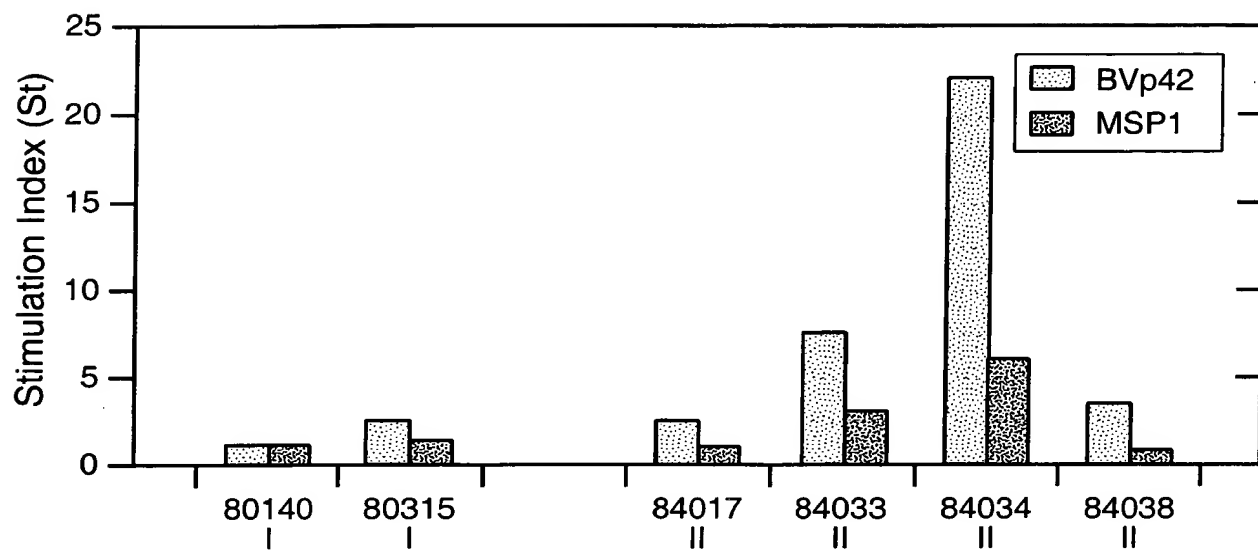


FIG._8D

**FIG._9**

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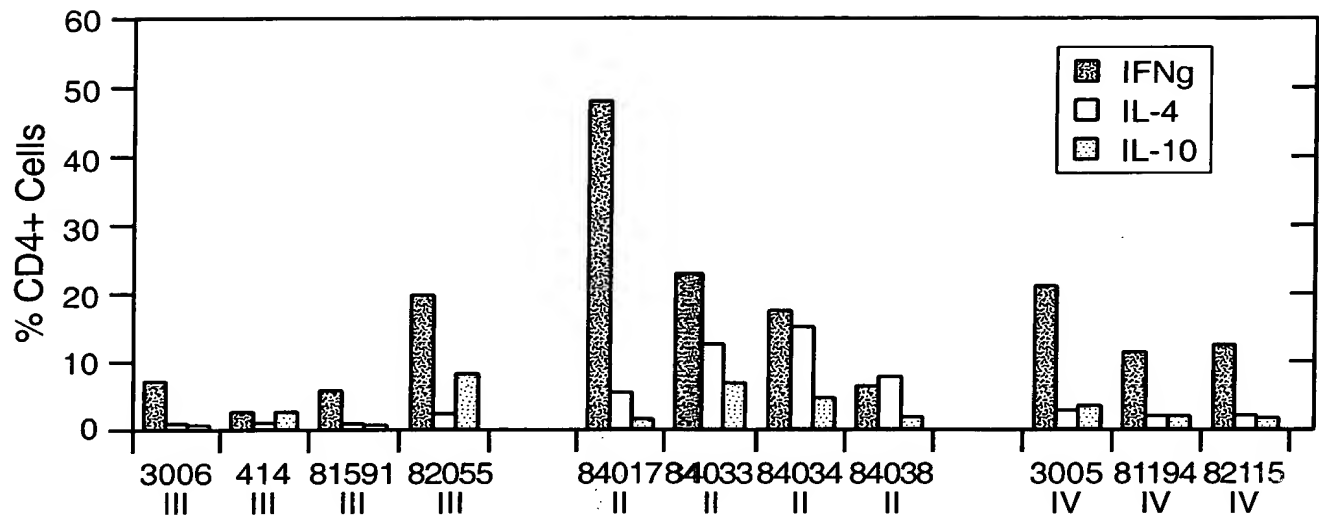


FIG. 10A

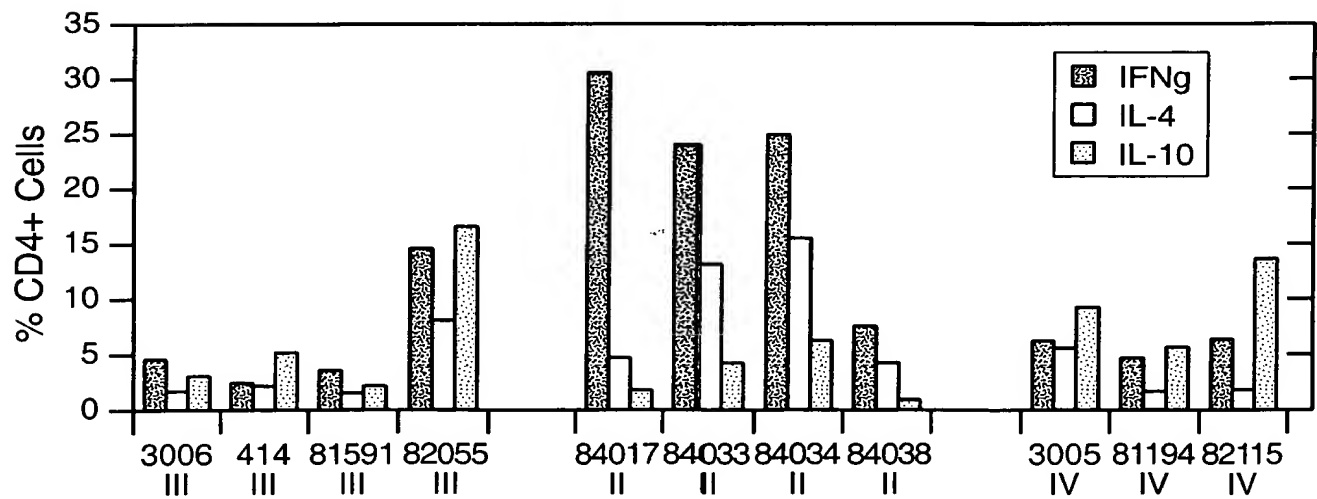


FIG. 10B

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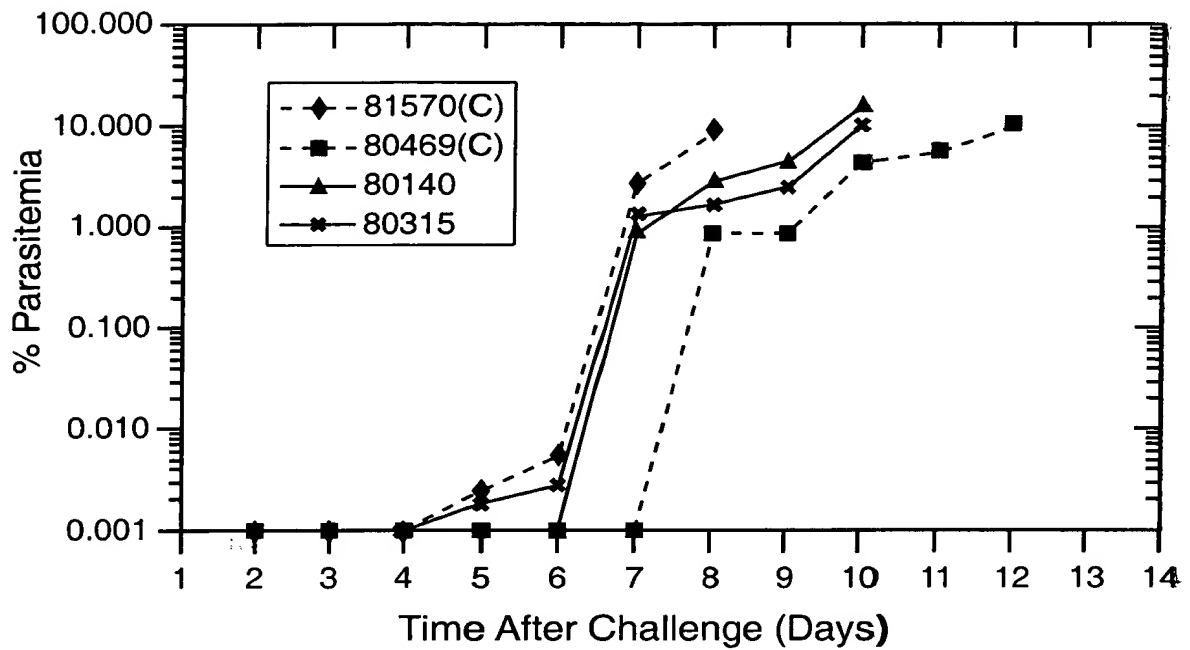


FIG. 11A

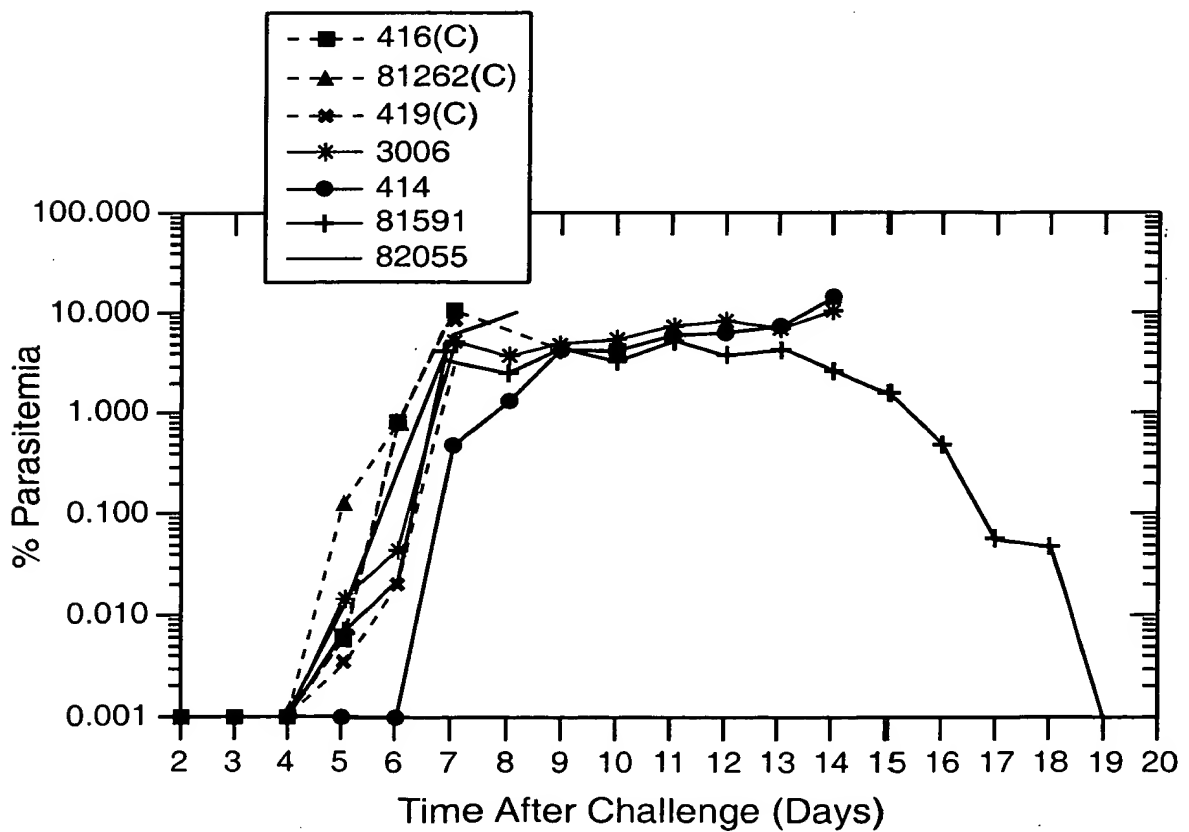


FIG. 11B

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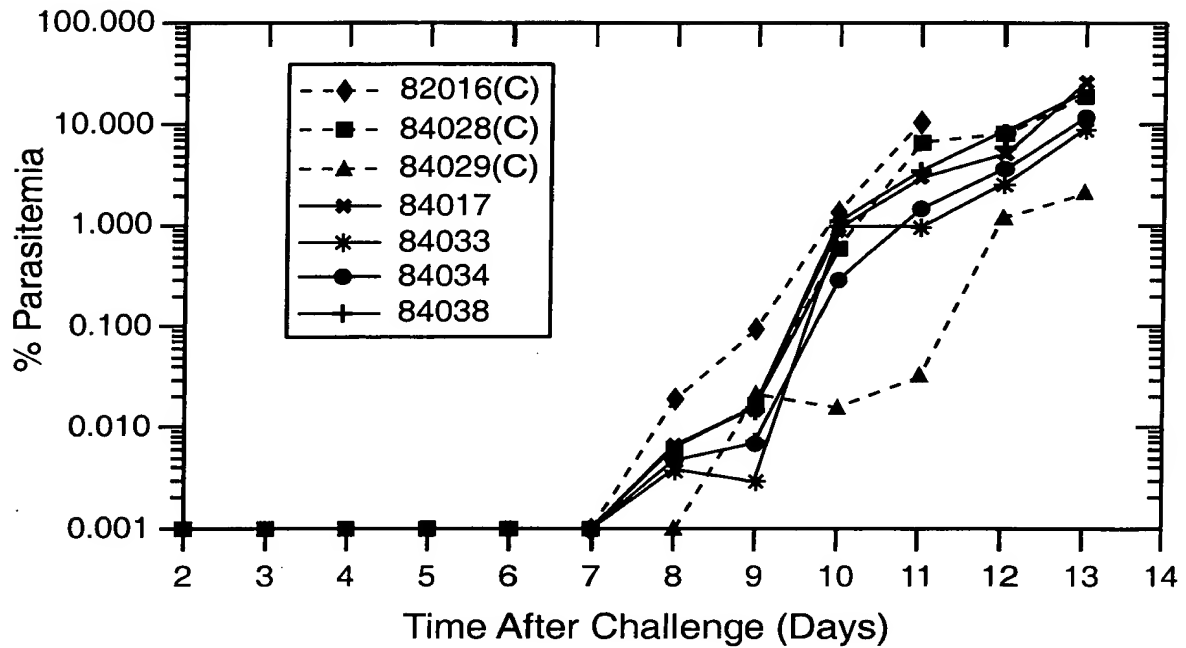


FIG. 11C

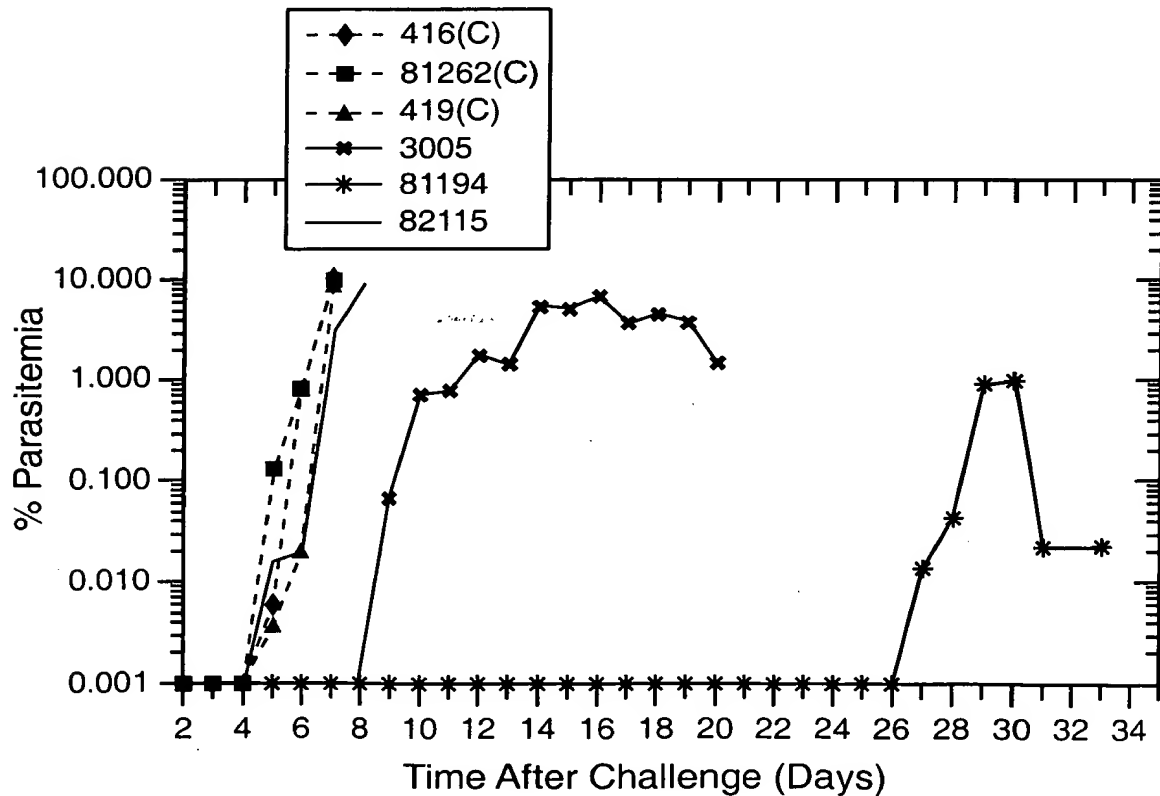


FIG. 11D

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DNA AND AMINO ACID SEQUENCE OF BVp42-M

attggatccactaaa

13 atgtggtccttggaagtgtctttttattctgggctgtcttggtgacc
M W S W K C L L F W A V L V T
58 gccactcctttgcacagcagcgatctctgttactatggacaacatc
A T L C T A A I S V T M D N I
103 ctcagtggccttcgagaacgagtagcagcgtaatctacctaagccc
L S G F E N E Y D V I Y L K P
148 cttgccggtgtctaccgttcattgaagaaacagatagaaaagaat
L A G V Y R S L K K Q I E K N
193 attttcacgttcaacctcaacctaaatgacatcctcaactcgcgc
I F T F N L N L N D I L N S R
238 ctcaagaagcgaaaatacttctcgcagctgttggaatccgacctt
L K K R K Y F L D V L E S D L
283 atgcaatttaagcacattagctctaacgagtagcatcatagaggac
M Q F K H I S S N E Y I I E D
328 agcttcaagctcttgaattcagaacagaagaacaccctcctaaag
S F K L L N S E Q K N T L L K
373 tcctacaaatacattaaggagtctgttgagaacgacatcaagttc
S Y K Y I K E S V E N D I K F
418 gcccaggaaggaattagctactatgagaaagtcctggctaaatac
A Q E G I S Y Y E K V L A K Y
463 aaggacgacttggaagcattaagaaggtaatacaagaagagaag
K D D L E S I K K V I K E E K
508 gaaaagtttccgagctctccaccacaaactcccccatcgctgca
E K F P S S P P T T P P S P A
553 aagaccgacgagcagaaaaaagaaagtaagttccttccattcctc
K T D E Q K K E S K F L P F L
598 accaacatcgaaactctatataacaacctggtgaacaagattgat
T N I E T L Y N N L V N K I D
643 gactacttaatcaacttgaaggcgaaaattaatgactgtaacgtc
D Y L I N L K A K I N D C N V
688 gaaaaggatgaagcccacgttaagatcaccaagctttccgatctc
E K D E A H V K I T K L S D L
733 aaagccatcgacgataagattgacctgtttaagaaccacaacgat
K A I D D K I D L F K N H N D
778 ttcgacgcaatcaaaaagttgatcaacgacgataactaagaaagac
F D A I K K L I N D D T K K D
823 atgcttggaactgctgtcgcagaggcttggtccaaaacttcccg
M L G K L L S T G L V Q N F P
868 aacaccattataagcaagctgatcgaaggaaagtttcaggatatg

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N T I I S K L I E G K F Q D M
913 ctgaacatctctcagcatcaatgcgtgaagaagcaatgtcccgag
L N I S Q H Q C V K K Q C P E
958 aattcagggttgcttccgccacttagacgaaaggagggaatgtaaa
N S G C F R H L D E R E E C K
1003 tgcctgctgaattataaacaggaaggagacaagtgcgtagagaat
C L L N Y K Q E G D K C V E N
1048 cctaaccacaacctgtaacgaaaataacggtggctgcgatgctgac
P N P T C N E N N G G C D A D
1093 gctaagtgtaccgaggaggacagcggttccaatggcaagaaaata
A K C T E E D S G S N G K K I
1138 acttgccaatgcacgaagcccgatagttaccctctcttcgacggt
T C E C T K P D S Y P L F D G
1183 atcttctgctcc
I F C S

ccacctcatcatcatcatcatcattaataagggtaccta
P P H H H H H H * *

FIG._12B

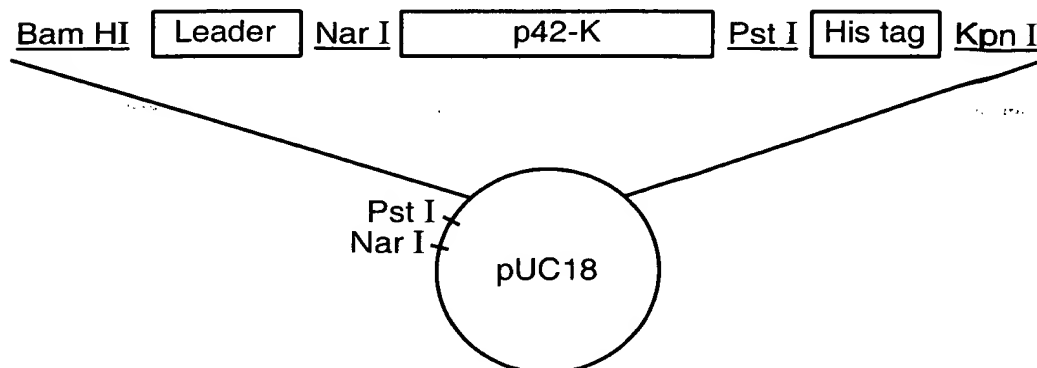


FIG._13

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DNA AND AMINO ACID SEQUENCE OF P42-K

1 GGATCCCT~~AAAA~~ATGTGGAGCTGGAAGTGCCTCCTCTTCTGGGCTGTCCTG
M W S W K C L L F W A V L
51 GTCACAGCCCACTCTGCACCGCGGGCGCCGCAGTAACTCCTTCCGTAAT
V T A T L C T A G A A V T P S V I
101 TGATAACATACTTTCTAAAATTGAAAATGAATATGAGGTTTTATATTTAA
D N I L S K I E N E Y E V L Y L
151 AACCTTTAGCAGGTGTTTATAGAAGTTTAAAAAACAATTAGAAAATAAC
K P L A G V Y R S L K K Q L E N N
201 GTTATGACATTTAATGTTAATGTTAAGGATATTTTAAATTCACGATTTAA
V M T F N V N V K D I L N S R F N
251 TAAACGTGAAAATTTCAAAAATGTTTTAGAATCAGATTTAATTCCATATA
K R E N F K N V L E S D L I P Y
301 AAGATTTAACATCAAGTAATTATGTTGTCAAAGATCCATATAAATTTCTT
K D L T S S N Y V V K D P Y K F L
351 AATAAAGAAAAAAGAGATAAATTCTTAAGCAGTTATAATTATATTAAGGA
N K E K R D K F L S S Y N Y I K D
401 TTCAATAGATACGGATATAAATTTTGCAAATGATGTTCTTGGATATTATA
S I D T D I N F A N D V L G Y Y
451 AAATATTATCCGAAAAATATAAATCAGATTTAGATTCAATTA~~AAAA~~AATAT
K I L S E K Y K S D L D S I K K Y
501 ATCAACGACAAACAAGGTGAAAATGAGAAATACCTTCCCTTTTAAACAA
I N D K Q G E N E K Y L P F L N N
551 TATTGAGACCTTATATAAAACAGTTAATGATAAAATTGATTTATTTGTAA
I E T L Y K T V N D K I D L F V
601 TTCATTTAGAAGCAAAAGTTCTAAATTATACATATGAGAAATCAAACGTA
I H L E A K V L N Y T Y E K S N V
651 GAAGTTAAAATAAAAGAACTTAATTACTTAAAAACAATTCAAGACAAATT
E V K I K E L N Y L K T I Q D K L
701 GGCAGATTTTAAAAAAAATAACAATTTTCGTTGGAATTGCTGATTTATCA~~A~~
A D F K K N N N F V G I A D L S
751 CAGATTATAACCATAATAACTTATTGACAAAGTTCCTTAGTACAGGTATG
T D Y N H N N L L T K F L S T G M



801 GTTTTGGAAAATCTTGCTAAAACCGTTTTATCTAATTTACTTGATGGAAA
V F E N L A K T V L S N L L D G N
851 CTTGCAAGGTATGTTAAACATTTTACAACACCAATGCGTAAAAAACAAT
L Q G M L N I S Q H Q C V K K Q
901 GTCCACAAAATTCTGGATGTTTCAGACATTTAGATGAAAGAGAAGAATGT
C P Q N S G C F R H L D E R E E C
951 AAATGTTTATTAAATTACAAACAAGAAGGTGATAAATGTGTTGAAAATCC
K C L L N Y K Q E G D K C V E N P
1001 AAATCCTACTTGTAACGAAAATAATGGTGGATGTGATGCAGATGCCAAAT
N P T C N E N N G G C D A D A K
1051 GTACCGAAGAAGATTCAGGTAGCAACGGAAAGAAAATCACATGTGAATGT
C T E E D S G S N G K K I T C E C
1101 ACTAAACCTGATTCTTATCCACTTTTCGATGGTATTTTCTGCAGTCATCA
T K P D S Y P L F D G I F C S H H
1151 TCATCATCATCATTAATAAGGTACC
H H H H * *

Underlined sequences represent restriction sites.

Bold letters represent alterations done to the leader sequence as described in the methods.

The boxed letter represents the original sequence where a mis-sense mutation to a cytosine occurred.

"*" represent stop codons.

FIG._14B

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1 2 3 4 5 6 7 8 9

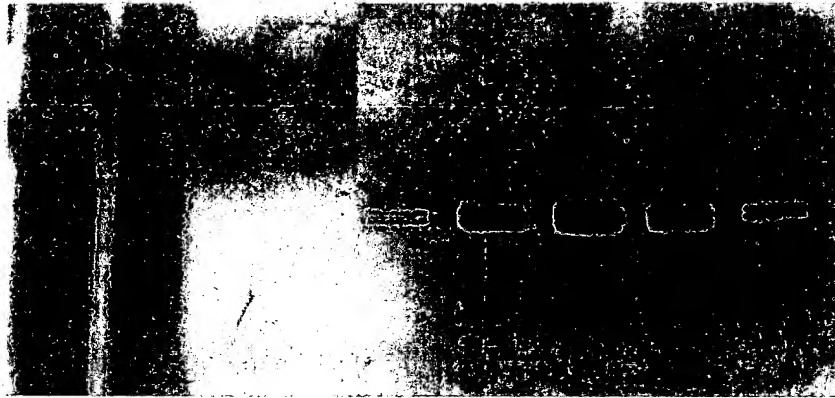


FIG._15

1 2 3 4 5 6 7 8



FIG._16

1 2 3 4 5 6 7 8

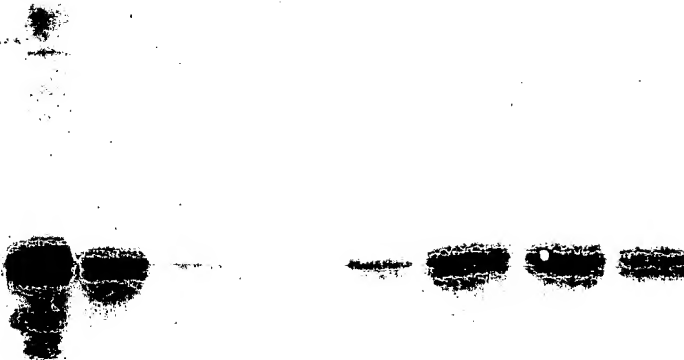
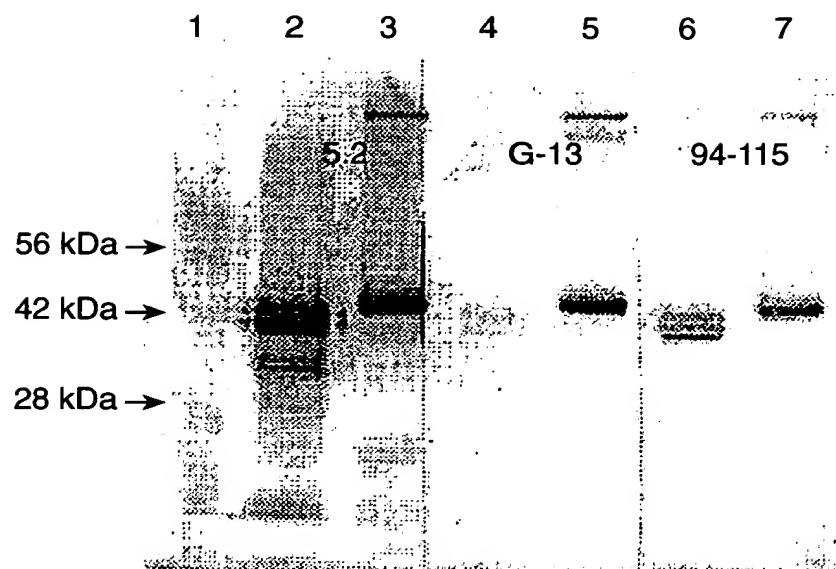
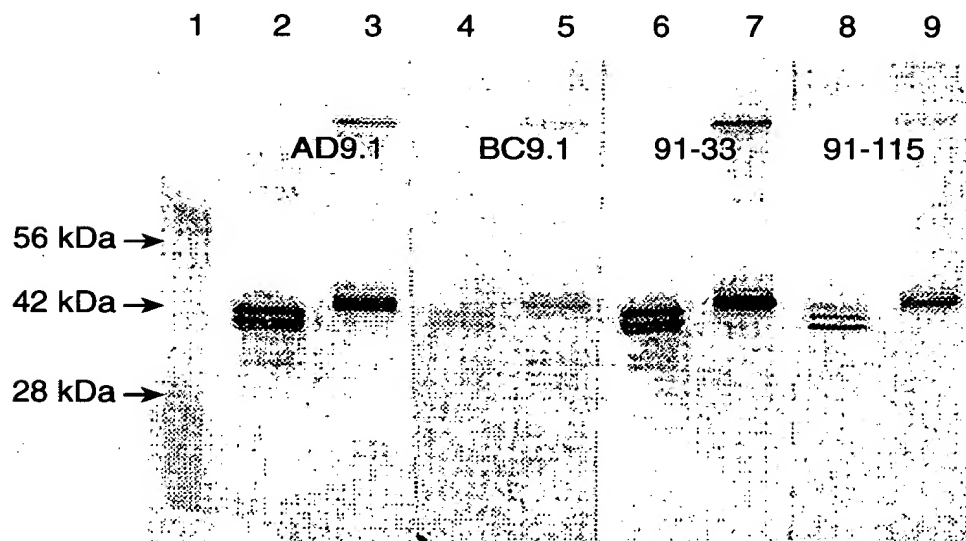


FIG._17

17698 U.S. PTO
102504

17698 U.S. PTO
102504

**FIG._18A****FIG._18B**